

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,  
Wyman, D., Ye, W. J., Zimmer, A. and Zou, M.  
Submitted 11-05-1999. Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 12, 2000 this sequence version replaced g1:6479010.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research  
Genome Center

Center code: MIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

----- Project Information -----

Center project name: L3517

Center clone name: L3517

----- Summary Statistics -----

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 121051 bases at least Q40

Consensus quality: 152215 bases at least Q30

Insert size: 167000; agarose-fp

Insert size: 185740; sum-of-contigs

Quality coverage: 3.5 in Q20 bases; agarose-fp

Quality coverage: 3.1 in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently  
\* consists of 51 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

```

* 1 1197: contig of 1197 bp in length
* 1198 1297: gap of 100 bp
* 1298 2601: contig of 1304 bp in length
* 2602 2701: gap of 100 bp
* 2702 3906: contig of 1205 bp in length
* 3907 4006: gap of 100 bp
* 4007 5023: contig of 1017 bp in length
* 5024 5123: gap of 100 bp
* 5124 6559: contig of 1436 bp in length
* 6560 6659: gap of 100 bp
* 6660 8178: contig of 1519 bp in length
* 8179 8278: gap of 100 bp
* 8279 9354: contig of 1076 bp in length
* 9355 9454: gap of 100 bp
* 9455 10758: contig of 1304 bp in length
* 10759 10858: gap of 100 bp
* 10859 12011: contig of 1153 bp in length
* 12012 12111: gap of 100 bp
* 12112 13508: contig of 1397 bp in length
* 13509 13608: gap of 100 bp
* 13609 14887: contig of 1279 bp in length
* 14888 14987: gap of 100 bp
* 14988 16156: contig of 1169 bp in length
* 16157 16256: gap of 100 bp
* 16257 17785: contig of 1529 bp in length
* 17786 17885: gap of 100 bp
* 17886 18947: contig of 1062 bp in length
* 18948 19047: gap of 100 bp
* 19048 20330: contig of 1283 bp in length
* 20331 20430: gap of 100 bp
* 20431 21914: contig of 1484 bp in length
* 21915 22014: gap of 100 bp
* 22015 23101: contig of 1087 bp in length
* 23102 23201: gap of 100 bp
* 23202 24447: contig of 1246 bp in length
* 24448 24547: gap of 100 bp

```

#### FEATURES

source

misc\_feature

```

* 24548 26032: contig of 1485 bp in length
* 26033 26132: gap of 100 bp
* 26133 28012: contig of 1880 bp in length
* 28013 28112: gap of 100 bp
* 28113 30280: contig of 2168 bp in length
* 30281 30380: gap of 100 bp
* 30381 31436: contig of 1056 bp in length
* 31437 31536: gap of 100 bp
* 31537 33906: contig of 2370 bp in length
* 33907 34006: gap of 100 bp
* 34007 35444: contig of 1438 bp in length
* 35445 35544: gap of 100 bp
* 35545 38284: contig of 2740 bp in length
* 38285 38384: gap of 100 bp
* 38385 40159: contig of 1775 bp in length
* 40160 40259: gap of 100 bp
* 40260 42089: contig of 1830 bp in length
* 42090 42189: gap of 100 bp
* 42190 43894: contig of 1705 bp in length
* 43895 43994: gap of 100 bp
* 43995 46499: contig of 2505 bp in length
* 46500 46599: gap of 100 bp
* 46600 48033: contig of 1434 bp in length
* 48034 48133: gap of 100 bp
* 48134 51777: contig of 3644 bp in length
* 51778 51877: gap of 100 bp
* 51878 55116: contig of 3339 bp in length
* 55117 55216: gap of 100 bp
* 55217 57721: contig of 2505 bp in length
* 57722 57821: gap of 100 bp
* 57822 61349: contig of 3528 bp in length
* 61350 61449: gap of 100 bp
* 61450 65218: contig of 3769 bp in length
* 65219 65318: gap of 100 bp
* 65319 68743: contig of 3425 bp in length
* 68744 68843: gap of 100 bp
* 68844 74044: contig of 5201 bp in length
* 74045 74144: gap of 100 bp
* 74145 78742: contig of 4598 bp in length
* 78743 78842: gap of 100 bp
* 78843 82807: contig of 3965 bp in length
* 82808 82907: gap of 100 bp
* 82908 87683: contig of 4776 bp in length
* 87684 87783: gap of 100 bp
* 87784 92706: contig of 4523 bp in length
* 92707 92806: gap of 100 bp
* 92807 99946: contig of 7140 bp in length
* 99947 100046: gap of 100 bp
* 100047 107272: contig of 7226 bp in length
* 107273 107372: gap of 100 bp
* 107373 115832: contig of 8460 bp in length
* 115833 115932: gap of 100 bp
* 115933 124872: contig of 8940 bp in length
* 124873 124872: gap of 100 bp
* 124873 134820: contig of 8868 bp in length
* 134821 134820: gap of 100 bp
* 134821 143495: contig of 8575 bp in length
* 143496 143595: gap of 100 bp
* 143596 152927: contig of 9332 bp in length
* 152928 153027: gap of 100 bp
* 153028 164076: contig of 11049 bp in length
* 164077 164176: gap of 100 bp
* 164177 173869: contig of 9633 bp in length
* 173870 173969: gap of 100 bp
* 173970 190740: contig of 16771 bp in length.

```

location/Qualifiers

1..190740 Homo sapiens

/db-xref="taxon:9606"

/clone="Rpl116C4"

/clone\_lib="RPl11 Human Male BAC"

1..1197

/note="assembly-fragment"

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misc_feature      13609..14887
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misc_feature      14988..16156
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misc_feature      16257..17785
                    /note="assembly-fragment"
misc_feature      17886..18947
                    /note="assembly-fragment"
misc_feature      19048..20330
                    /note="assembly-fragment"

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Query Match      100.0%; Score 52; DB 2; Length 190740;
Best Local Similarity 100.0%; Pred. No. 2,5e+22;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 CTCCTCCGATTCGATTCGAGTCAGTCAGTAGTATCTGTCGACA 52
DB 68067 CTCCTCCGATTCGATTCGAGTCAGTCAGTAGTATCTGTCGACA 68118

```

```

RESULT 4
AC117652/c      203193 bp      DNA      linear      HTG 06-AUG-2002
LOCUS      Mus musculus clone RP23-291D3, WORKING DRAFT SEQUENCE, 41 ordered
DEFINITION      pieces.
AC117652      AC117652.2 GI:22123330
VERSION      HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
KEYWORDS      house mouse.
SOURCE      Mus musculus
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
REFERENCE      Birren,B., Nusbaum,C. and Lander,E.
AUTHORS      Birren,B., Nusbaum,C. and Lander,E.
TITLE      Mus musculus, clone RP23-291D3
JOURNAL      Unpublished
AUTHORS      2 (bases 1 to 203193)
REFERENCE      Birren,B., Linton,L., Nusbaum,C., Lander,E., All,A., Allen,N.,
Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavsky,L.,
Boukhalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,T.,
Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
Cook,A., Cooke,P., DeRellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,
Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,
Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., LaRoque,K., Lamzarez,R.,
Landers,T., Lehoczy,J., Levine,R., Lindblad-Toh,K., Liu,G.,
Maclean,C., Macdonald,P., Major,J., Margulis,N., Matthews,L.,
McCarthy,M., McKean,P., McKernan,K., Meldrum,J., Meneus,L.,
Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R.,
Nolte,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,
Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollard,V.,
Raymond,C., Retta,R., Rieback,W., Riley,R., Rise,C., Rogov,P.,
Roman,J., Roselli,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,
Seaman,J., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J.,

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TITLE      JOURNAL
JOURNAL      Submitted (10-Apr-2002) Whitehead Institute/MIT Center for Genome
REFERENCE      Research, 320 Charles Street, Cambridge, MA 02141, USA
AUTHORS      3 (bases 1 to 203193)

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COMMENT      TITLE
JOURNAL      Submitted (10-Apr-2002) Whitehead Institute/MIT Center for Genome
COMMENT      Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT      On Aug 6, 2002 this sequence version replaced gi:20128416.
COMMENT      All repeats were identified using RepeatMasker:
COMMENT      Smit, A.F.A. & Green, P. (1996-1997)
COMMENT      http://ftp.genome.washington.edu/RM/RepeatMasker.html

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----- Genome Center
Center: Whitehead Institute/MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: 291.D-3
Center clone name: L21684
----- Summary Statistics
Sequencing vector: plasmid; R/Y: 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 190811 bases at least Q40
Consensus quality: 195133 bases at least Q30
Consensus quality: 197994 bases at least Q20
Insert size: 230000; agarose-fp
Insert size: 199193; sum-of-contigs
Quality coverage: 4.1 in Q20 bases; sum-of-contigs
Quality coverage: 4.8 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 41 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1
957 1056: gap of 100 bp
1057 1812: contig of 756 bp in length
1813 1912: gap of 100 bp
1913 2571: contig of 659 bp in length
2572 2671: gap of 100 bp
2672 3534: contig of 863 bp in length
3535 3634: gap of 100 bp
3635 4507: contig of 873 bp in length
4508 4607: gap of 100 bp
4608 5874: contig of 1267 bp in length
5875 5974: gap of 100 bp

```